

OM protein - protein search, using sw model

Run on: March 17, 2003, 08:47:27 ; Search time 35 seconds
(without alignments)

Scoring table: BL2SUM62

Gapop 10.0 , Gapext 0.5

Title: US-10-010-227-3

Perfect score: 4055

Sequence: 1 MPGAEASTPOTLYDKVLQAHV.....KAVPVPTNRGEGKEPLEW 778

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2432.5	60.0	711	3 Q9BY5	Q9BY5 Yarrowia li
2	1636.0	40.3	469	16 Q92176	Q92176 rhizobium m
3	1611.0	39.7	469	16 Q8YJC9	Q8YJC9 brucella m
4	1586.0	39.1	475	16 Q8BY9	Q8BY9 agrobacteri
5	1567.5	38.7	469	16 Q98EF1	Q98EF1 rhizobium l
6	1563.0	38.5	448	2 Q9EV53	Q9EV53 rhizobium m
7	1562.0	38.5	479	16 Q9ABNO	Q9ABNO caulobacter
8	1549.5	38.2	469	16 Q97Z15	Q97Z15 neisseria m
9	1507.5	37.2	474	16 Q9JU82	Q9JU82 neisseria m
10	1498.0	37.0	474	16 Q9PAH3	Q9PAH3 pseudomonas
11	1493.0	36.8	469	16 Q8XXK3	Q8XXK3 xylella fas
12	1493.0	36.8	469	16 Q8XAO0	Q8XAO0 ralstonia s
13	1469.5	36.2	466	16 Q8ZLH0	Q8ZLH0 escherichia
14	1452.5	35.8	476	16 Q9kP81	Q9kP81 yersinia pe
15	1425.5	35.2	467	16 Q9kP80	Q9kP80 vibrio chol
16	1396.0	34.4	472	16 Q9kP80	Q9kP80 bacillus ha

17 1385.5 34.2 476 16 Q86534 streptomyce

18 1354.5 33.4 466 16 Q85072 buchnera ap

19 1354.5 33.4 469 2 Q85065 buchnera ap

20 1315.5 32.4 448 2 Q8VF9Q buchnera ap

21 1311.5 32.3 470 16 Q9PLW1 campylobact

22 1290.5 31.8 466 16 Q91293 buchnera ap

23 1283.5 31.7 462 16 Q92A26 Q92a26 listeria in

24 1282.5 31.6 456 16 Q99SJ3 Q99s3 staphylococ

25 1280.5 31.6 442 2 Q8VH1 Q8vh1 buchnera ap

26 1279.5 31.6 462 16 Q8Y5R7 Q8y5r7 listeria mo

27 1275.5 31.5 443 2 Q8EV10 Q8ev10 buchnera ap

28 1271.5 31.4 444 2 Q8VG8 Q8vg8 buchnera ap

29 1259.5 31.1 443 2 Q8EVG5 Q8evg5 buchnera ap

30 1253.5 30.9 443 2 Q8EV6 Q8ev6 buchnera ap

31 1252.5 30.9 442 2 Q8EV13 Q8ev13 buchnera ap

32 1244.5 30.7 436 2 Q8AJ49 Q8aj49 buchnera ap

33 1240.5 30.6 442 2 Q8EVH7 Q8evh7 buchnera ap

34 1238.5 30.5 436 2 Q8AJ47 Q8aj47 buchnera ap

35 1238.5 30.5 473 16 Q82RJ0 Q82rj0 salmonella ap

36 1226.5 30.5 443 2 Q8EVH4 Q8evh4 buchnera ap

37 1220.5 30.3 436 2 Q92ND5 Q92nd5 thermus the

38 1227.5 30.3 456 2 Q94IM3 Q9aim3 streptococc

39 1225.5 30.2 444 2 Q8YX02 Q8yx02 anaerobacter ap

40 1222.5 30.1 433 2 Q99Q99 Q99q99 buchnera ap

41 1217.5 30.0 473 16 Q82RJ0 Q82rj0 salmonella ap

42 1211.5 29.9 442 2 Q8EVG2 Q8evg2 buchnera ap

43 1209.5 29.8 472 2 Q92ND5 Q92nd5 thermus the

44 1194.5 29.5 456 2 Q94IM3 Q9aim3 streptococc

45 1172.5 28.9 467 16 Q8YX02 Q8yx02 anaerobacter ap

46 1170.5 28.9 418 2 Q9AJ50 Q9aj50 buchnera ap

47 1055.5 26.3 369 2 Q91Q6 Q91q6 rhizobium e

48 639.5 17.3 418 17 Q8TVE2 Q8tve2 methanopyru

49 660.5 16.3 424 17 Q8TFL1 Q8tfl1 methanosaer

50 656.5 16.2 424 16 Q97KEB Q97keb clostridium

51 641.0 15.8 431 16 Q9RT6 Q9rt6 deinococcus

52 640.5 15.8 659 16 Q97W24 Q97w24 thermotoga

53 637.5 15.7 423 17 Q9U207 Q9u207 pyrococcus

54 637.5 15.5 415 16 Q8YMA6 Q8yma6 rhizobium e

55 612.5 15.1 641 16 Q8RCFB Q8rcfb thermococcus

56 599.0 14.8 642 16 Q97KEB Q97keb clostridium

57 597.5 14.7 417 16 Q9WZ24 Q9wz24 thermotoga

58 595.5 14.7 417 16 Q9WZ24 Q9wz24 thermotoga

59 586.5 14.5 420 16 Q98E51 Q98e51 rhizobium 1

60 576.5 14.2 422 16 Q97EE0 Q97ee0 clostridium

61 570.5 14.1 509 10 Q94AR8 Q94ar8 rabidopsis

62 562.0 13.9 420 17 Q97QZ3 Q97qz3 methanosaer

63 562.0 13.9 661 17 Q9HMFL Q9hmf1 halobacteri

64 560.5 13.8 216 16 Q8UBR0 Q8ubr0 agrobacteri

65 558.5 13.8 509 10 Q9P014 Q9p014 arabidopsis

66 555.5 13.7 509 16 Q92LA1 Q92la1 rhizobium m

67 552.0 13.6 721 3 Q9UT74 Q9ut74 schizosach

68 544.0 13.4 213 16 Q9U081 Q9ju81 neisseria m

69 542.0 13.4 212 16 Q9HZ4 Q9hz4 pseudomonas

70 542.0 13.4 213 16 Q9IZ16 Q9iz16 neisseria m

71 541.5 13.4 418 16 Q9NYC7 Q9nyc7 thermotoga

72 536.5 13.2 72 16 Q96VU1 Q96vu1 aspergillus

73 535.0 13.2 216 16 Q8XXX4 Q8xxx4 ralstonia s

74 533.0 13.1 201 2 Q8R98 Q8r98 methylobact

75 523.5 12.9 418 16 Q92NE0 Q92ne0 thermus the

76 519.0 12.8 215 16 Q9PAK1 Q9pak1 xylella fas

77 513.0 12.7 202 16 Q9BN1 Q9bni caulobacter

78 512.0 12.6 434 16 Q9RTY9 Q9rty9 deinococcus

79 511.5 12.6 418 16 Q8DDK2 Q8ddk2 thermomaer

80 506.0 12.5 201 16 Q8Z913 Q8z913 salmonella

81 500.5 12.3 201 16 Q9GCN8 Q9gcn8 pastuerella

82 498.0 12.3 200 16 Q9RP80 Q9rpb80 vibrio chol

83 492.0 12.1 201 16 Q8XA01 Q8xa01 escherichia

84 482.0 11.9 768 4 Q9UZG0 Q9uzg0 homo sapien

85 474.5 11.7 780 4 Q8TQ06 Q8tq06 homo sapien

86 474.0 11.7 200 16 Q8Z1H1 Q8z1h1 yersinia pe

87 473.0 11.7 780 11 Q99K10 Q99k10 mus musculu

88 472.5 11.7 780 11 Q9RP34 Q9rpb34 rattus norv

89 472.5 11.7 787 11 Q9NF51 Q9nfx1 diosphilia

90	470.5	11.6	778	3	074699	aspergillus
91	467	11.5	194	16	Q9K8F1	bacillus ha
92	463	11.4	3	Q9P7D4	schizosacch	
93	457	11.3	809	3	Q9HEA5	neurospora
94	455	11.2	788	5	Q9NG03	daphnia pul
95	447	11.0	415	17	Q8ZWM1	pyrobaculum
96	442.5	10.9	747	2	Q8RP87	bacteroides
97	442	10.9	683	5	Q9VIE8	dersophilida
98	441	10.9	402	17	Q8TN29	methanopyru
99	440	10.9	415	17	Q974R0	sulfolobus
00	438	10.8	196	2	Q9AIM2	streptococc

ELEMENTS

DR	PROSITE; PS00450; ACONITASE_1; UNKNOWN_1.
DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
KW	lyase; Complete proteome.
SQ	SEQUENCE 469 AA; 5094 MW; 22A2F7D040645726 CRC64;
Query Match	40.3%; Score 1636; DB 16; Length 469; Best Local Similarity 66.0%; Pred. No. 3 3e-102; Matches 313; Conservative 57; Mismatches 96; Indels 8; Gaps 3; Mismatches 96; Indels 8; Gaps 3;
QY	6 STPQTYDVKVQAHVYDEKLDGTIVYIDRHLVHEVTSPOAEGLNAGRKVRPPCTLA 65
Db	2 SAPRTIYDVKIDMDHLYDSDGTCUCLYIDRHLVHEVTSPOAEGLNAGRKVRPPCTLA 61
QY	126 EQGFTLPGTTVCGDSHTSTHGAFGALAHGIGTSEVHVLATQCLTRRSKMRQVDE 185
Db	117 EQGFTLPGMTVCGDSHTSTHGAFGALAHGIGTSEVHVLATQCLTRRSKMRQVDE 176
QY	186 LARGVSSKDVLHAIGITGAGGTGAVIEFCGSVTSMSARMSCNMSTEGGARAGMV 245
Db	177 LPGVYAKDILAIATGIGTGTAGGTGAVIEFCGSVTSMSARMSCNMSTEGGARAGLV 236
QY	246 APDEITPEYLKRPARKYDSPEWHKATOYWKNLQSDPGAKYDIDPDAKDIVPILWG 305
Db	237 APDETFEYIKKOPRKPGEA-WDRAYEWKTLHDEGAHYDRVWVLDAAANLPPIVSWG 294
QY	306 TSPEDVVPIGTGVVPDPDFTATEAKKADGRMRMQLYQMGKLAGTPEMDPVDKFIGSCNSR 365
Db	295 SSPEDVVSVQGVVPNPDDIODETKRISKWRLADYMGKPGKTKIDIAKDRVFIGSCNGR 354
QY	366 IEDRLAAAVWVKRKPKPNVKSAMVPGSGLYKTOAEEBEGLKIPEAGFEEAREAGCSCM 425
Db	355 IEDRLAAVWVKRKPKPNVKSAMVPGSGLYKTOAEEBEGLKIPEAGFEEAREAGCSCM 413
QY	426 LGMNPDTIAPQRCASTSNRNFEGRGROGGGRTHLMSVMAAAGIVKLADVR 479
Db	414 LAMNDRDKLPGRCASTSNRNFEGRQDFKGRTHLSPAMAAAAGVAGHFVDIR 467
RESULT 3	
Q8YJC9	PRELIMINARY; PRT; 469 AA.
ID	Q8YJC9; 08YJC9; PRELIMINARY; PRT; 469 AA.
AC	08YJC9; 01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).
GN	BME0157.
OS	Bacillus
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC	Bacteriaceae; Brucellae.
OX	NCBI_TaxID:29459;
RN	[1] NCBI_TaxID:176299;
RP	SEQUENCE FROM N.A.
RX	STRAIN=>GM / ATCC 34456 / BIOTYPE 1;
RX	MEDLINE=20020109; PubMed=11756688;
RA	DelVecchio V.G., Kapitar V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., D'Souza M., Bernal A., Mazur M., Golsman E., Jelkow E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyriides N., Overbeek R.; "The genome sequence of the facultative intracellular pathogen Brucella melitensis.;" <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:443-448 (2002).
DR	EMBL; AE009458; AAL51339.1; -; InterPro; IPR001030; Aconitase_N.
DR	InterPro; IPR004430; IeuC.
DR	PFM; PF00330; aconitase_1.
DR	PRINTS; PR00415; ACONITASE.
DR	Prodrom; PDD000511; Aconitase_N; 1.
DR	TIGRFAMS; TIGR00170; leuc; 1.
DR	PROSITE; PS00450; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
KW	lyase; Complete proteome.
SQ	SEQUENCE 469 AA; 5092 MW; 14442D94C40BCDF CRC64;
Query Match	39.7%; Score 1611; DB 16; Length 469; Best Local Similarity 66.8%; Pred. No. 1 6e-100; Matches 316; Conservative 51; Mismatches 98; Indels 8; Gaps 3; Mismatches 98; Indels 8; Gaps 3;
QY	6 STPQTYDVKVQAHVYDEKLDGTIVYIDRHLVHEVTSPOAEGLNAGRKVRPPCTLA 65
Db	2 SAPRTIYDVKIDMDHLYDSDGTCUCLYIDRHLVHEVTSPOAEGLNAGRKVRPPCTLA 61
QY	126 EQGFTLPGTTVCGDSHTSTHGAFGALAHGIGTSEVHVLATQCLTRRSKMRQVDE 185
Db	117 EQGFTLPGMTVCGDSHTSTHGAFGALAHGIGTSEVHVLATQCLTRRSKMRQVDE 176
QY	186 LARGVSSKDVLHAIGITGAGGTGAVIEFCGSVTSMSARMSCNMSTEGGARAGMV 245
Db	177 LPGVYAKDILAIATGIGTGTAGGTGAVIEFCGSVTSMSARMSCNMSTEGGARAGLV 236
Db	177 LPAGVTKDIVIAIGBIGTAGGTGVVYEAGEATRSLSMGRMTICNMSTEGGARAGLV 236
QY	246 APDEITPEYLKRPARKYDSPEWHKATOYWKNLQSDPGAKYDIDPDAKDIVPILWG 305
Db	237 APDETFEYIKKOPRKPGEA-WDRAYEWKTLHDEGAHYDRVWVLDAAANLPPIVSWG 294
QY	306 TSPEDVVPIGTGVVPDPDFTATEAKKADGRMRMQLYQMGKLAGTPEMDPVDKFIGSCNSR 365
Db	295 SSPEDVVSVQGVVPNPDDIODETKRISKWRLADYMGKPGKTKIDIAKDRVFIGSCNGR 354
QY	366 IEDRLAAAVWVKRKPKPNVKSAMVPGSGLYKTOAEEBEGLKIPEAGFEEAREAGCSCM 425
Db	355 IEDRLAAVWVKRKPKPNVKSAMVPGSGLYKTOAEEBEGLKIPEAGFEEAREAGCSCM 413
QY	426 LGMNPDTIAPQRCASTSNRNFEGRGROGGGRTHLMSVMAAAGIVKLADVR 479
Db	414 LAMNDRDKLPGRCASTSNRNFEGRQDFKGRTHLSPAMAAAAGVAGHFVDIR 467
RESULT 4	
Q8BY9	PRELIMINARY; PRT; 475 AA.
ID	Q8BY9; 08BY9; PRELIMINARY; PRT; 475 AA.
AC	08BY9; 01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	3-isopropylmalate dehydratase, large subunit.
GN	LEUC OR ATU2709 OR AGR_C_4910.
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970)
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC	OC
OC	Rhizobiaceae; Rhizobium.
OC	NCBI_TaxID:176299;
RN	[1] NCBI_TaxID:176299;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21608550; PubMed=11743193;
RA	Wood D.W., Setubal J.C., Kaul R., Monk D.E., Kitajima J.-P., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovée D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A., Romero P., Gordon D., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Gordon M., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chanley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W., "The genome of the natural genetic engineer Agrobacterium tumefaciens C58;" <i>Science</i> 294:2317-2323 (2001).
RA	[2]

MEDLINE=20222556; PubMed=10761919;							
RA	Partill J., Achttman M., James K.D., Bentley S.D., Churcher C., Klei S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moulé S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;	RT	"Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 22491."	RT	"Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 22491."	RL	Nature 404:502-506 (2000).
DR	EMBL; AL162756; CABBA4686.1; ~.	DR	IntPro; IPR001030; Aconitase_N.	DR	InterPro; IPR004430; LeucC.	DR	PFam; PF00330; Aconitase_1.
DR	PRINTS; PRO00451; ACONITASE.	DR	ProDom; PD000051; Aconitase_N; 1.	DR	TIGR48M; TIGR00170; leucC_1.	DR	PROSITE; PS00050; ACONITASE_1; PROSITE; PS01244; ACONITASE_2; 1.
DR	DR	DR	DR	DR	DR	KW	
SEQUENCE	469 AA;	50733 MW;	89AE349827DA25DB CRC64;	38.1%; Score 1545.5; DB 16; Length 469; Best Local Similarity 63.4%; Pred. No. 4.2e-96; Matches 301; Conservative 62; Nsmatches 103; Indels 9; Gaps 3	3	Complete proteome.	
Qy	7 TPAQTLQAHVYDEKLGDGTIVLTYIDRDLHVLHETVSPQAEGRLNRAGRKVRPDPCTLAT	66	2 TAQTLQDVKWNHVVREEDGTVLIDRDLHVLHETVSPQAEGRLNRAGRKVRPDPCTLAT	61	67 TDHNPVPTSRKALKDIAPIKEDDSRTQCVTLEENVKERG-VTYFGLSIDKROGIVHVG	125	
Db	62 ADHNPPT----GDWDKQIOPDSKLQVDTLDNIKEKGALAYFPFMKGQGIVHVMGP	115	126 EQGATLPGTIVVCCDSHTSHTGAFGALLARGIGTSEVETHYLATQCLITKRSKNNRIVQDGE	185	116 EQGATLPGTIVVCCDSHTSHTGAFGALLAHIGTSEVETHYLATQCLITKSKMSLIAVDGK	175	
Qy	186 LAPGVSSKKVYVLAHIGIICTAGGTGAVIEFCGSVIRSLSEARMSICNMSIEGGARAGMV	245	176 LKAGVTTKDVAKDVALVYIQQTAGGTGTYATEFGGEAIRSLMEGRNLTNNAIEAGARSIV	235	246 APDEITFEYLGKGRPLAKYDSDPEWPKHATQYWNKLOSDPEGAKYDIDVFDIAKDIYPTLNG	305	
Db	236 AVDQTTIDYVKDKPFAPEEAA--WDKAVEYWRTLVSDEGAEVKERYRFNAEDELQPVITNG	293	306 TSPEDVVPITGVPPDPEPATEAKKADGRMLQYMGKQGTPMEDIIVPKVFIGSCTNSR	365	236 AVDQTTIDYVKDKPFAPEEAA--WDKAVEYWRTLVSDEGAEVKERYRFNAEDELQPVITNG	293	
Qy	294 TSPEMVLDDSSKVPNPAEETDPYKRSGMERALEYMGLEGTPLNEIPDVFIGSCTNSR	353	294 TSPEMVLDDSSKVPNPAEETDPYKRSGMERALEYMGLEGTPLNEIPDVFIGSCTNSR	353	366 IEDLRAAAAVVGRKKPAVNPSAMVPGSGLVKTQAEPEGLDKIFEEAGFEWREAGCSMC	425	
Db	354 VDIREAAIAKDKRKKAANQVRLVPGSLVQEAKRGLDKIFIEAGFEWREAGCSMC	413	354 VDIREAAIAKDKRKKAANQVRLVPGSLVQEAKRGLDKIFIEAGFEWREAGCSMC	413	426 LGMNPDLAPOERCASTSNRNFEGROGAGGRTHLMSPYMAAAGIVGKLADEVKLL	480	
Qy	414 LAMNADRTPQCASTSNRNFEGROGAGGRTHLVSAMAAAATVGRFTDIRMM	468	414 LAMNADRTPQCASTSNRNFEGROGAGGRTHLVSAMAAAATVGRFTDIRMM	468	426 LGMNPDLAPOERCASTSNRNFEGROGAGGRTHLMSPYMAAAGIVGKLADEVKLL	480	
Db	414 LAMNADRTPQCASTSNRNFEGROGAGGRTHLVSAMAAAATVGRFTDIRMM	468	414 LAMNADRTPQCASTSNRNFEGROGAGGRTHLVSAMAAAATVGRFTDIRMM	468	426 LGMNPDLAPOERCASTSNRNFEGROGAGGRTHLMSPYMAAAGIVGKLADEVKLL	480	
RESULT 10	Q9HZA3	PRELIMINARY;	Q9HZA3	PRELIMINARY;	Q9HZA3	PRELIMINARY;	
ID	Q9HZA3	PRT;	AC	Q9HZA3;	AC	PRT;	
DR	01-MAR-2001	(TREMBrel.	DT	01-MAR-2001	16, Created)	01-MAR-2001	
DT	(TREMBrel.	16, Last sequence update)	DT	(TREMBrel.	21, Last annotation update)	01-JUN-2002	
DE	3-isopropylmalate dehydratase large subunit		DE	3-isopropylmalate dehydratase large subunit			
GN	LEIC		GN	PA3121			
Pseudomonas aeruginosa			OS	Pseudomonas aeruginosa			
Bacteria; Proteobacteria; gamma subdivision			OC	Bacteria; Proteobacteria; gamma subdivision			
Pseudomonadaceae			OC	Pseudomonadaceae			
NCBI_TaxID=287;			OX	NCBI_TaxID=287;			

RP
SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RN [1]
RX MEDLINE=20437337; PubMed=0984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Barber R.L., Goitier S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Iory S., Olson M.V.;
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL: AE004736; AAG0509.1; --.
DR InterPro: IPR001030; Aconitase_N.
DR InterPro: IPR00430; Leuc.
DR Pfam: PF00310; aconitase_1.
DR PRINTS: PRO0415; ACONITASE.
DR PRODOM: PD00051; ACONITASE_1; 1.
DR TIGRFAMS: TIGR00170; leuC; 1.
DR PROSITE: PS00050; ACONITASE_1; 1.
DR PROSITE: PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 474 AA; 51042 MW; 7B4A0F6500C228EC CRC64;
Query Match 37.2%; Score 1507.5; DB 16; Length 474;
Best Local Similarity 62.5%; Pred. No. 1.6e-93;
Matches 295; Conservative 61; Mismatches 113; Indels 3; Gaps 2;
QY 9 QTYLKDQVLAQHVDKEUDGTVLLYIYDRHLVHEVTSQAFEGLRNAGRKVRPDCATTD 68
Db 4 KTYLKDQVLAQHVDKEUDGTVLLYIYDRHLVHEVTSQAFEGLRNAGRKVRPDCATTD 63
QY 6 9 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENVKFGVTFFGLSDKRGQVHVGPEQ 128
Db 6 4 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENVKFGVTFFGLSDKRGQVHVGPEQ 122
QY 129 FTLPGTTVVCQGSDHTSSTHGAFGALAGIGTSEVERVHATOCILTKESKNMTIQVDFELAP 188
Db 123 ATLPGMWVVCQGSDHTSSTHGAFGALAGIGTSEVERVHATOCILVKAKMKNMLVVEGRLLPA 182
QY 189 GVSSKQVVLHATIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAPD 248
Db 183 GVTAKDVLAVIGRIGTAGGNGHATIEFGASATRDLSTGRMTCNMSEAGARVGLVAVD 242
QY 249 EITFEVYKGRPLAKPVYSPENHATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTS 308
Db 243 QKTDIVYKGRPPA- SAEQWQDAVACWQGLVSDADARFDTVELDAQKQPVQNSGTS 300
QY 309 EDVYPTTQVVPDPETRATTEAKQKADGRMLQWQGLKACTPMDIIPVDRVFIQSCNTNSIED 368
Db 301 ENVLAVDQVNVPDPARESDDPIKRGSTIERALKWYGLRPNQAITDQLDRVFIQSCNTNSIED 360
QY 369 LRAAAVVKGRKKPAPNVSAMVPGSGLVKTQAEEGDQKTFEEAGFWRERANGCSMCLGM 428
Db 361 LRAAAEVARGKVAATIQKALVPGSGLVKEQAEKGIDRIFTEAGFWRERANGCSMCLAM 420
QY 429 NPDILAQRCRCASTSNRNFEGSQQGAGRTHLSPVMAAAGVGKLAQDVRL 480
Db 421 NPDRLSEGGCASTSNRNFEGQGAGGTHLSPAMAAQAAVNGRFIDVRL 472
RESULT 11
Q9PAX0 PRELIMINARY; PRT; 474 AA.
ID Q9PAX0; PRELIMINARY; PRT; 474 AA.
AC 01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
DT 3-isopropylmalate dehydratase large subunit.
GS XP2375.
OS *Xylella* fastidiosa.
OS *Xylella* fastidiosa.
OS *Bacteri*; *Proteobacteria*; *gamma subdivision*; *Xanthomonas* group;
OC *Xylella*.

OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=0365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman G.H., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kempfer E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lemos M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."
RL Nature 406:151-159 (2000).
DR EMBL: AE004747; AAF83174.1; --.
DR InterPro: IPR001030; Aconitase_N.
DR InterPro: IPR00430; Leuc.
DR Pram; PFO0310; aconitase_1.
DR PRINTS; PRO0415; ACONITASE.
DR PRODOM; PD00051; Aconitase_N; 1.
DR TIGRFAMS; TIGR00170; leuC; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 474 AA; 51183 MW; 998DFDFB2B23750 CRC64;
Query Match 37.0%; Score 1498.5; DB 16; Length 474;
Best Local Similarity 63.1%; Pred. No. 6.4e-93;
Matches 298; Conservative 52; Mismatches 119; Indels 3; Gaps 2;

QY 9 QTYLKDQVLAQHVDKEUDGTVLLYIYDRHLVHEVTSQAFEGLRNAGRKVRPDCATTD 68
Db 4 KTYLKDQVLAQHVDKEUDGTVLLYIYDRHLVHEVTSQAFEGLRNAGRKVRPDCATTD 63
QY 69 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENVKFGVTFFGLSDKRGQVHVGPEQ 128
Db 64 HNVPTTSRKALKDIASTIKEDDSRTQCVTLEENVKFGVTFFGLSDKRGQVHVGPEQ 122
Db 123 ATLPGMWVVCQGSDHTSSTHGAFGALAGIGTSEVERVHATOCILVKAKMKNMLVVEGRLLPA 182
QY 189 GVSSKQVVLHATIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNNSIEGGRAGRMVAPD 248
Db 183 GVTAKDVLAVIGRIGTAGGNGHATIEFGASATRDLSTGRMTCNMSEAGARVGLVAVD 242
QY 249 EITFEVYKGRPLAKPVYSPENHATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTS 308
Db 243 EITFEVYKGRPLAKPVYSPENHATQWKNLQSDPGKAYDIDVFDIADKIVPTLWTGTS 300
QY 309 EDVYPTTQVVPDPETRATTEAKQKADGRMLQWQGLKACTPMDIIPVDRVFIQSCNTNSIED 368
Db 301 ENVLAVDQVNVPDPARESDDPIKRGSTIERALKWYGLRPNQAITDQLDRVFIQSCNTNSIED 360

Qy	369	LRAAAAYVKGKKAPVNKSAMVYVGSLVYKTOAREBGLDKIFERAGFWEAEGGSMCLGM	428	Db	295	EMVVS1EDRVPDPDKERKDPVKRNAMMERALEYMAQPNVAIGDIRDKVFIGSCTNSRIED	354
Db	361	LRAAEYVKGKTYASTVQAMVYVGSLVYKTOAEEBGLDKIFERAGFWEAEGGSMCLAM	420	Qy	369	LRAAAAVAVK--GRKKRPENVKSAMVYVGSLVYKTOAEEBGLDKIFERAGFWEAEGGSMCL	426
Qy	429	NPDILAPDERRCASTSNRNPFGRCAGGRTLMSPVMAAGIYVKLADYKL	480	Db	355	MRAAAWVQKLQKRIASNVKLAMVYVGSLVYKTOAEEBGLDKIFERAGFWEAEGGSMCL	414
Db	421	NPDKLGSSEHCASTSNRNPFGRCAGGRTLVSFAMAAAAVAGHFDREM	472	Qy	427	GMNPDPDLPQERCASSTSNRNPFGRCAGGRTLMSPVMAAGIYVKLADYKL	480
				Db	415	AMNADLPLEPGERCASTSNRNPFGRCAGGRTLVSFAMAAAALLEGHFDREM	468
RESULT 12							
Q8XXXX3		PRELIMINARY;		PRT;	469	AA.	
AC	Q8XXX3;						
DT	01-MAR-2002	(TREMBLrel.	20, Created)				
DT	01-JUN-2002	(TREMBLrel.	21, Last annotation update)				
DE	Probable 3-isopropylmalate dehydratase (Large subunit)	protein					
GN	LEUC	OR RSC1990 OR RS01558.					
OS	Ralstonia solanacearum (Pseudomonas solanacearum).						
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia group;						
NCBI_TaxID	305						
RN							
RP	SEQUENCE FROM N.A.						
RC	STRAIN=GMI1000;						
RX	Medline-21681879; PubMed=11123852;						
RA	Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,						
RA	Arlat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,						
RA	Chandler M., Choine M., Claude-Renard C., Cunnac S., Demange N.,						
RA	Siguiere P., Trehault P., Whalen M., Wincker P., Levy M.,						
RA	Weissenbach J., Boucher C.A., Robert C., Saurin W., Schleier T.,						
RA	"Genome sequence of the plant pathogen Ralstonia solanacearum."						
RL	Nature 415:497-502(2002).						
DR	InterPro; IPR001030; Aconitase_N.						
DR	InterPro; IPR004430; Leuc.						
DR	InterPro; IPR004430; aconitase.						
DR	PRINTS; PR00415; ACONITASE.						
DR	PRODOM; PD000511; Aconitase_N.						
DR	TIGRFaNs; TIGR00101; Leuc.						
DR	PROSITE; PS00450; ACONITASE_1.						
DR	PROSITE; PS01244; ACONITASE_2.						
KW	Lysase; Complete proteome.						
SQ	SEQUENCE 469 AA; 50796 MW;	B451E96E44788AAE	CRC64;				
Query Match	36.8%	Score 1493;	DB 16;	Length 469;			
Best Local Similarity	63.5%	Pred. No. 1..5-92;					
Matches 301; Conservative	53;	Mismatches 110;	Indels 10;	Gaps 3;			
Qy	9	QTYLYDKVLOQAHVYDEKLDTGTVLIDRHLVHEYTSPOAEGFLRNAGRKVRPFDCTLATTID	68	Db	3	KTYLYKLFDQHVVYPAENETPLLYDRHLVHEYTSQAEGFLRAHGPVRQGKTFATMD	62
Db	3	KTYLYKLFDQHVVYPAENETPLLYDRHLVHEYTSQAEGFLRNAGRKVRPFDCTLATTID	62	Qy	69	HNVPTFSRALKDIAFSIKEDDSRTOCVLLEENKEFVYTFGLSDKROQIVHYVIGPQG	128
Qy	69	HNVPTFSRALKDIAFSIKEDDSRTOCVLLEENKEFVYTFGLSDKROQIVHYVIGPQG	128	Db	63	HNVSTC---KDINAC-GEMARIQMQLIKNCRFVGVELDNPYQGIVHMGGBQG	116
Db	63	HNVPTFSRALKDIAFSIKEDDSRTOCVLLEENKEFVYTFGLSDKROQIVHYVIGPQG	116	Qy	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQLTRSKRMRIQVGDGELAP	188
Qy	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQLTRSKRMRIQVGDGELAP	188	Db	117	ATLPGMTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQLTRSKRMRIQVGDGELAP	176
Db	117	ATLPGMTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQLTRSKRMRIQVGDGELAP	176	Qy	189	GVSSKDQVVLHAGLIGTGTAGGTGAVIEFGCSVIRSLSMARMSICNMSTEGGARAGMVPD	248
Qy	189	GVSSKDQVVLHAGLIGTGTAGGTGAVIEFGCSVIRSLSMARMSICNMSTEGGARAGMVPD	248	Db	177	GTAKD1VLAIGKIGTAGGTGAMERGCSAIALSMGRMTVCNMAGMVGVD	236
Db	177	GTAKD1VLAIGKIGTAGGTGAMERGCSAIALSMGRMTVCNMAGMVGVD	236	Qy	249	EITFEYLKGRLPLAKPKYDSPEWKAHATQYKWNQLQSDPGAKYDIDVFDIDVPLTWGCTSP	308
Qy	249	EITFEYLKGRLPLAKPKYDSPEWKAHATQYKWNQLQSDPGAKYDIDVFDIDVPLTWGCTSP	308	Db	237	DITLEYLKGRPPFAPOQ--GVEWQAVYVRSLHDEGARFDHYVLLRABEIRPQSWGTSP	294
Qy	237	DITLEYLKGRPPFAPOQ--GVEWQAVYVRSLHDEGARFDHYVLLRABEIRPQSWGTSP	294	Db	309	EDVVPVIGVVPDPETFATEAKKADGRMRMLQYMGKLAGTPMEDIIVDVKYFIGSCTNSRIED	368
Qy	309	EDVVPVIGVVPDPETFATEAKKADGRMRMLQYMGKLAGTPMEDIIVDVKYFIGSCTNSRIED	368	Qy	129	FTLPGTIVVCGDSHTSHTGAGLAFGIGTSEVHVLATQLTRSKRMRIQVGDGELAP	188

Db 117 VTLPGMTIVCGSDHTATHGAFGALAFGIGTSEVHEVLAQTQKGRAKTMKIEVQGKAP 176
 Qy 189 GVSSKDVTHAIGIIGTAGGTGAVIEPGSVRSLNEMARICNSIEGARAGMYPD 248
 Db 177 GITAKDVLVLAIGTKTSAAGGTGHVVERGGEATRDLNEMGRMTLNCNAIEEMGAKAGLAP 236
 Qy 249 EITPEYIKGRPLAKYDPEWKHATQWKNLQSDPGAKYDIDVFDADKDIVPLTGTS 308
 Db 237 ETTENYVKGRLHAPK- GKDFDFAVAYWKTQDGEATFDTWVTLQEEISPOVTWNTP 294
 Qy 309 EDVVPITGVVPDPETFAEAKADGRMLQYMGKAGTPMEDIIPVDKVFIISCTNRIED 368
 Db 295 GQVISVNDNIPDPAFDPVERASAEGKALAYWGLKPGILTEVAIDKVFQGSCTNSKED 354
 Qy 369 LRAAAVVKGRKAKPNKSAAMYPGVQVLTQAEEDKTFEEAGFWRAGCSCMIGM 428
 Db 355 LRAAAEAKGRKVAPGQ-AIIVPGSPEVKQAEAGDKEFAGEFWRLPGCSMILAM 413
 Qy 429 NPDILAPQERCASNRNFEGROGAGGRTHLMSPVMAAAGIVGKLAIVRKL 480
 Db 414 NNDRLNPGERCASNSNFEGROGRRGRTLIVSPAMAAAATVIGHFADIRNI 465
 RESULT 14
 Q8ZIHO ID Q8ZIHO PRELIMINARY; PRT; 476 AA.
 AC Q8ZIHO:
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).
 GN LBCUC OR YP06531.
 OS Yersinia.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / BTOVAR ORIENTALIS;
 RX MEDLINE=2140413; PubMed=1586360;
 RA Chillingworth T., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley D.S., Brooks J., Cerdeno-Tarago A.M.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karpashev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutledge B.,
 RA Simmonds M., Skeatley J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527 (2001).
 DR EMBL; AJ4143; CAC89388.1; --.
 DR InterPro; IPR001030; Aconitase_N.
 DR InterPro; IPR00430; LeuC.
 DR Pfam; PF00330; aconitate; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR PRODOM; PD00511; Aconitase_N; 1.
 DR TIGRFAM; TIGR00170; LeuC; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.
 DR KW Lyase; Complete proteome.
 SQ SEQUENCE 476 AA; 5089 MW; 052D8EB2165P5E74 CRC64;
 Query Match 35.8%; Score 1452; DB 16; Length 476;
 Best Local Similarity 59.2%; Pred. No. 8.98-90;
 Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;
 Qy 1 MGAESTHTQTLVYKVLQHWDKLDGTWLYIDRHLTHEVTSPOAEGFLRNAGKVRP 60
 Db 1 MGTTSSQSOPTLYQKLYDHLVHRAPNETPPLYIDRHLHEVTSPOAEGFLRNAGKVRP 60
 Qy 61 DCLATTPHNVPSTSKALKDIAPIKDSRQCYTLEENVEKPGVYFLGSLDKRCIV 120
 Db 61 GKTFTAMDHNVSTQ---KDINA--SEBMARIQMQLKJNCAEFGVSYLYDLMHFOCIV 114

Qy 121 HVTGPEQGFTLPGTIVCGSDHTATHGAFGALAFGIGTSEVHEVLAQTQKGRAKTMKIEVQGKAP 180
 Db 115 HVIGPBOGMWTLPGMTIVCGSDHTATHGAFGSLAFGIGTSEVHEVLAQTQKGRAKTM 174
 Qy 181 QVGDGELAPGVSSKDVVHAIGTIGTAGGTGAVIEPGVSIISMEARMSICNSIEGGA 240
 Db 175 EYNGTVGAGITAKDVLIAIGKTGSAAGTGHVVEFGSATEALSMGGRMTLNCNAIEGMA 234
 Qy 241 RAGMVADEITEBYKGRPLAKYDPEWKHATQWKNLQSDPGAKYDIDVFDADKIVP 300
 Db 235 KAGIVADPDTTFAYLKGRQFAP- -TGEQWEGQSVAYWTRLKSDADAQDTIVLDAADI 292
 Qy 301 TLTWGTSPEDVWVPTGVVPDPETFAEAKADGRMLQYMGKAGTPMEDIIPVDKVFIGS 360
 Db 293 QVWGTGTPQVIAVNOITPAPESPSPDVERASAEGKALAYMDLRPGKLTVEAIDKVFQGS 352
 Qy 361 CTNSRIEDLRAAAAVVKGRKAKPNKSAWVPGSGLVQVLTQABEEGLDKIFEEAGFEEREA 420
 Db 353 CTNSRIEDLRAAAVAKGRKVAKGQ-AIIVPGSPEVKQAEAGLKDIFTAAGFWRRLP 411
 Qy 421 GCSMCLGKNDPDLAPQERCASNRNFEGROGAGRTHLMSPVMAAAGIVGKLAIVRKL 480
 Db 412 GCSMCLAMNDRLEPGERCASNSNFEGROGRRGRTLIVSPAMAAAATVIGHFADIREL 471
 Qy 481 TDYKASPH 488
 Db 472 S--ATH 476
 RESULT 15
 Q8KPB1 ID Q8KPB1 PRELIMINARY; PRT; 467 AA.
 AC Q8KPB1:
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 3-isopropylmalate dehydratase, large subunit.
 GN VC492.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE 01;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Douson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Bhattacharya M.D., Vamathevan J., Bass S., Qin H., Drago I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.,
 RA RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*";
 RL Nature 406:477-483 (2000).
 DR EMBL; AF004318; AFM95634.1; --.
 DR TIGR; VC2492; --.
 DR InterPro; IPR001030; Aconitase_N.
 DR InterPro; IPR004430; LeuC.
 DR Pfam; PF00330; aconitate; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR PRODOM; PD00511; Aconitase_N; 1.
 DR TIGRFAM; TIGR00170; LeuC; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 467 AA; 50185 MW; 4F760714FA85ADD CRC64;

Query Match 35.2%; Score 1425.5; DB 16; Length 467;
 Best Local Similarity 58.9%; Pred. No. 5.3e-88;
 Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;

DR	InterPro; IPR01030; Aconitase_N.	DR	PRINTS; PRO0415; ACONITASE.
DR	InterPro; IPR00430; LeuC.	DR	ProDom; P0000511; Aconitase_N; 1.
DR	PF00330; aconitase; 1.	DR	TIGRFAMS; TIGR00170; leuC; 1.
DR	PRINTS; PRO0415; ACONITASE.	DR	PROSITE; PS00450; ACONITASE; 1.
DR	ProDom; P000511; Aconitase_N; 1.	DR	PROSITE; PS01244; ACONITASE_2; 1.
DR	TIGRFAMS; TIGR00170; LeuC; 1.	KW	Plasmid.
DR	PROSITE; PS00450; ACONITASE; 1.	FT	NON-TER.
DR	PROSITE; PS01244; ACONITASE_2; 1.	SEQUENCE	448 AA; 448 AA; 4936 MW; 0137DA4418C29779 CRC64;
KW	Isomerase; Plasmid.	SEQUENCE	469 AA; 52426 MW; 4094EC232646228B CRC64;
SEQUENCE	469 AA;	Query Match	33.4%; Score 1354; DB 2; Length 469;
Best Local Similarity	56.6%; Pred. No. 3.6e-33;	Best Local Similarity	32.4%; Score 1315.5; DB 2; Length 448;
Matches	267; Conservative 76; Mismatches 119; Indels 10; Gaps 5;	Matches	57.1%; Pred. No. 1.3e-80;
Db	3 KTLXKYYDHIVHBEKNNNSILYDLHLHEVTSQAFSLRMRNNSYRQPKCTFATMD 62	Db	260; Conservative 70; Mismatches 116; Indels 9; Gaps 4;
Qy	69 HNVPTTSRKALKDIASTIKEDDSRTQVTCYCLEENYKEFGTYFGLSDKROGIVHVGPEQ 128	Qy	9 QTLYDKVLQAHVVDKEDGTVLILYIDRHLVHEVTSQAFGLRNAGRKVVRPDCTLATTD 68
Db	63 HNVSTTS---KD-NA---SSMAAKIQMQLIKNCBENFALYDINNPQGIVHVGPEQ 116	Db	3 KTLXKYYDHIVHBEKNNNSILYDLHLHEVTSQAFSLRMRNNSYRQPKCTFATMD 62
Qy	129 FTLPGTTVYCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188	Qy	69 HNVPTTSRKALKDIASTIKEDDSRTQVTCYCLEENYKEFGTYFGLSDKROGIVHVGPEQ 128
Db	117 LTLPSSTTVCGDSHTSTHGFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188	Db	63 HNVSTTS---QDIN---SGSMARQVQMOPLIKNSYDLYDKNPHQGIVHVGPEQ 116
Qy	189 GVSSKDVVLHAIGLITGAGGTGAVIEFCGSVIRSLMSARMSIGNMSIEGGARAGMVPD 248	Qy	129 FTLPGTTVYCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188
Db	177 FVPAKDLILIFIGKLGSSGAGYIEFCGSVIRSLMSARMSIGNMSIEGGARAGMVPD 248	Db	117 MTLPGMTIVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188
Qy	249 EITPEYLKGRLPLAKYDSPWEHRAKATQYWNQLOSPDGAKYDIDVFDIAKDIVP TLWGTSP 308	Qy	189 GVSSKDVVLHAIGLITGAGGTGAVIEFCGSVIRSLMSARMSIGNMSIEGGARAGMVPD 248
Db	237 ETIYLKNNKRYSPK--NWKWDSAIRYWKLTVIDBNALDFKEFFDISPDTISPOV TWGTSP 294	Db	117 MTLPGMTIVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188
Qy	309 EDVVPITGVVYGPDPETFATEAKKADGRRMLQYMGKLAGTTPMEDI PVDKVFIGSCTNSRIED 368	Qy	189 GVSSKDVVLHAIGLITGAGGTGAVIEFCGSVIRSLMSARMSIGNMSIEGGARAGMVPD 248
Db	295 DQVLISNEKIPDFNSFKDTSIKDLSRACNMDLKPGSYLKNIKDVKIGSCTNSRIED 354	Db	117 MTLPGMTIVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLIKRSKMRQIVDGE LAP 188
Qy	369 LRAAAVVKGRKKAAPNVSAMVPGSGLYKVTQREBEGLKDIFEEAGFEMR EACGCSMCLGM 428	Qy	249 EITPEYLKGRLPLAKYDSPWEHRAKATQYWNQLOSPDGAKYDIDVFDIAKDIVP TLWGTSP 308
Db	355 LRSAAATLKKNNKTSKNTK-AIVPGSGSYKNOAEKGDKIFIDAFGEWRLPGCSMCLGM 413	Db	237 ETIYLKNNKRYSPK--NWKWDSAIRYWKLTVIDBNALDFKEFFDISPDTISPOV TWGTSP 294
Qy	429 NPDLAPQERCASTSNRNFEGROGAGGRTHLMSPVMAAAGTIVGKLADVRKL 480	Qy	309 EDVVPITGVVYGPDPETFATEAKKADGRRMLQYMGKLAGTTPMEDI PVDKVFIGSCTNSRIED 368
Db	414 NNDKLSDGERCASTSNRNFEGROGAGGRTHLMSPVMAAAGTIVGKLADVRKL 464	Db	295 DQVLISNEKIPDFNSFKDTSIKDLSRACNMDLKPGSYLKNIKDVKIGSCTNSRIED 354
RESULT 21			
Q9FLW1	Q9FLW1	Q9FLW1	Q9FLW1
ID	Q9FLW1	ID	Q9FLW1
AC	Q9FLW1	AC	Q9FLW1
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Isopropylmalate dehydratase large subunit (Fragment).	DE	Isopropylmalate dehydratase large subunit (EC 4.2.1.33).
GN		GN	LCBIC OR CJI17C.
OS		OS	Campylobacter jejuni.
OC		OC	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.CTC 11168;
RC	SEQUENCE FROM N.A.	RC	STRAIN=NCTC 11168;
RC	SEQUENCE FROM N.A.	RC	MDLINE=20150912; PubMed=10689204;
RC	SEQUENCE FROM N.A.	RA	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
RC	SEQUENCE FROM N.A.	RA	"The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences.";
RC	SEQUENCE FROM N.A.	RL	Nature 403:665-668 (2000).
RC	SEQUENCE FROM N.A.	DR	EMBL; AL133079; CAB3703.1; -
RC	SEQUENCE FROM N.A.	DR	InterPro; IPR001030; Aconitase_N.
RC	SEQUENCE FROM N.A.	DR	InterPro; IPR00430; LeuC.
RC	SEQUENCE FROM N.A.	DR	InterPro; IPR00330; aconitase; 1.
RC	SEQUENCE FROM N.A.	DR	InterPro; IPR001030; Aconitase_N.

DR	InterPro; IPR004430; leuC.
DR	pFam; PF00330; aconitase; 1.
DR	PRINTS; PRO0415; ACONITASE.
DR	ProDom; PD00511; Aconitase_N; 1.
DR	TIGRFAMS; TIGR00170; leuC; 1.
DR	PROSITE; PS01244; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; 1.
KW	Complete proteome.
SEQUENCE	470 AA; 51930 MW; A63877597C846ADB CRC64;
Query Match	32.3%; Score 1311.5; DB 16; Length 470; Best Local Similarity 55.8%; Pred. No. 2.7e-80; Matches 264; Conservative 65; Mismatches 131; Indels 13; Gaps 4;
QY	9 QTLIDKVIQAHVVEDBKLDGTVLILYDRILVHEVTSPOAFEGIRNAGRKVRPDTLTD 68
Db	5 KTLIYEVKPVDAHVYVEGKQBLPLIVDRILHHEVTSPOAFSGLKMKRVARADLTATID 64
QY	69 HNVPTTSR--KALKDIASTFIKEDDSRTQCVTLEENVKERGVTYFGISDKRQGIHVWIGP 126
Db	65 HDVSTKSMIDLACSDMA----KEQITLIMONTKERGVRLIGLGDNQGITHIVE 116
QY	127 QGFTLPLGPTWVCGSHTSTHGAFAGLAAGFTSEVHVTATCITKRSKMRITQDGEI 186
Db	117 LGFTLPLGVTLVCGDSHTATGAGFALAFGIGTSEVHVTATCITKRSKMRITQDGEI 176
QY	187 APGSSKDVVLHAIGIGTAGGTGAVIEFGSVIRSLMSARMSLCNSTEGGARAGMYA 246
Db	177 QKGVYTKDILYLLAQYGTGAKTGYAIEFGELRNLSBARMTLCNMATEFGAKVGMIA 236
QY	247 PDETFEYIYKGRPLAPKYSPEWHKATQWKNLQSDPGAKYDIDVFDIPIVLTWTG 306
Db	237 PDETFEYIYKGRPLAPKYSPEWHKATQWKNLQSDPGAKYDIDVFDIPIVLTWTG 294
QY	307 SPEDVPTGTVVDPDPTFATEAKKADGRMLQYMLKAGTPMEDIPVKVFIGSTCNRI 366
Db	295 NPSQVIGIDKEPKTSDFKQSEOKSLDALYYVNLQDQVIEKGKIDIVFIGSTNGRL 354
QY	367 EDLRAAAVAVKGKKAPNPKNSAMVPGSGVKTQABEGGLDIFEEAGFWREREAGCSMCL 426
Db	355 EDLKAADILKGKRIHKNVK-ALTVPGSMQVRKEABNLGLDKIFIEAGCEWRYAGCSMCL 413
QY	427 GMNPDPILLAPQERCASNSRNRFGRQGAGGRTHLMSYMAAGIVGKLAURK 479
Db	414 GMNDKANSQVRVASTNSRNRFVGROGKGSTHLMSPASAACAIBGICDNRK 466
RESULT 22	
ID	031293 PRELIMINARY; PRT; 466 AA.
AC	031293; (TREMBrel. 05, Created)
DT	01-JAN-1998 (TREMBrel. 05, Last sequence update)
DT	01-JAN-1998 (TREMBrel. 05, Last annotation update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	3-isopropylmalate dehydratase subunit.
GN	LEUC.
OS	Buchnera aphidicola.
OG	Plasmid pB751.
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.
RN	[1] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=CLIP 11262 / SEROVAR 5A;
RX	PubMed=11679669;
RA	Glaser P., Frantz L., Buchrieser C., Rusniok C., Amend A.,
RA	Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA	Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA	Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA	Entian K.-D., Fischi H., Garcia-del Portillo F., Gaillard P.,
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA	Jones L.-M., Kaest J., Kieft J., Kuhn M., Kunst F., Kurupkat G.,
RA	Madueno E., Maitourna A., Mata Vicente J., Ng E., Nedjari H.,
RA	Nordahl G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA	Reimel B., Rose M., Schieterer T., Simoes N., Tizre A.,
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT	"Comparative genomics of <i>Listeria</i> species.";
RL	Science 294:849-852(2001).
DR	TIGRFAMS; TIGR00170; leuC; 1.
DR	PROSITE; PS00450; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; 1.
KW	Plasmid.
SEQUENCE	466 AA; 51930 MW; A63877597C846ADB CRC64;
SQ	Query Match 31.8%; Score 1290.5; DB 2; Length 466; Best Local Similarity 55.3%; Pred. No. 6.9e-7; Mismatches 137; Indels 9; Gaps 4;
QY	9 QTLIDKVIQAHVVEDBKLDGTVLILYDRILVHEVTSPOAFEGIRNAGRKVRPDTLTD 68
Db	3 QTLXKLVNHSIYEDKVNLPVYIDLILVHEVTSPOAFESLKNNKKRIVHAPIK-TFATMD 62
QY	69 HNVPTTSRALKDIASTFIKEDDSRTQCVTLEENVKERGVTYFGISDKRQGIHVWIGP 128
Db	63 HNVTKINK---ISASGKA-AQIQMQLINNCKDFNKLKLYLHINQGIVWIGP 116
QY	129 FTPLGTTVVGSDSTSTHGAFAGLAAGFTSEVHVTATCITKRSKMRITQDGEI 188
Db	117 LTLPQMTVCGDSHTSTHGAFGTLAFLGICSEVHVTATCITKRSKMRITQDGEI 176
QY	189 GVSXKDVVLHAIGIGTAGGTGAVIEFGSVIRSLMSARMSLCNSTEGGARAGMYA 248
Db	177 YITAKDVLVLYIYKVGTAFTGTVVFESEGETTENLTMEGRMTICNNVIEGAKSGLIAD 236
QY	249 EITBVKLGRPLAPKYSPEWHKATQWKNLQSDPGAKYDIDVFDIPIVLTWTG 308
Db	237 ATTYYKLKLPYAPKE-KMKALEYWKNLKKNDAKDPTKIVFDPDVSQIEPQITWGTNP 294
QY	309 EDVPIITGTVVDPDPTFATEAKKADGRMLQYMLKAGTPMEDIPVKVFIGSTCNRI 368
Db	295 SQTINITESNPDPRKINNIDQKATEKALKYMNLPKNQMINLVWDKVFIGSTCNRIED 354
QY	369 LRAAAVAVKGKKAPNPKNSAMVPGSGVKTQABEGGLDIFEEAGFWREREAGCSMCL 428
Db	355 LRIASKIKNKKVAKITK-AIVPGSKLVKIQAKREGDKIFIFAGFEWRILPGCSMCLAM 413
QY	429 NPDIIAPQERCASNSRNRFGRQGAGGRTHLMSYMAAGIVGKLAURK 480
Db	414 NDDKLNKRGERCASISNRNFEDRQERGGRTHLVLISITAAAIAFGYFVDIKNI 465

us-10-010-227-3.rapt

RT	(<i>Buchnera</i>). "
RL	J. Bacteriol. 183:785-790 (2001).
DR	EMBL; AFR197453; AAG31394; 1; -.
DR	InterPro; IPR01030; Aconitase_N.
DR	IntertPro; IPR00430; LeuC.
DR	PFAM; PF00330; aconitase; 1.
DR	PRINTS; PRO0415; ACONITASE.
DR	ProDom; PD00051; Aconitase_N; 1.
DR	TIGRFAMS; TIGR00170; LeuC; 1.
DR	PROSITE; PS00450; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; 1.
DR	Plasmid.
KW	
FT	NON_TER 442
FT	SEQUENCE 442 AA; 49589 MW; TACBEB7267AC18982 CRC64;
SQ	

Search completed: March 17, 2003, 08:50:17
Job time : 50 secs

Job time : 50 secs

